This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims

1. (original) A method of determining a sequence of a nucleic acid polymer, comprising the steps of:

(a) obtaining data traces from a plurality of channels of an electrophoresis detection apparatus, each channel detecting the products of a DNA sequencing reactions;

(b) combining the data traces by a process comprising the steps of:

(i) applying a cross-correlation coefficient to each of the four data traces to yield four refined traces, wherein the cross-correlation coefficient compares each of the traces with an ideal, Gaussian-shaped peak and wherein the refined traces have narrower peaks than the corresponding data traces;

(ii) combining the four refined traces to yield a composite trace;

(c) detecting peaks in the composite trace by a process that is independent of peak spacing; and

(d) determining the sequence of the nucleic acid polymer by assigning basecalls to the peaks.

2. (original) The method of claim 1, wherein the data traces have been preprocessed.

3. (original) The method of claim 2, wherein preprocessing comprises the steps of:

(i) obtaining unprocessed data traces from a plurality of channels of an automated electrophoresis detection apparatus, each channel detecting the products of a DNA sequencing reactions;

(ii) identifying begin and end points in the unprocessed data;

(iii) establishing a baseline in the unprocessed data,

(iv) subtracting the baseline from the unprocessed data to generate the baseline-corrected data; and

(v)　　separating the baseline-corrected data to generate the data traces, the separating step comprising spectral or leakage separation.

4.　　(original) The method of claim 1, wherein the electrophoresis detection apparatus uses slab gel electrophoresis; tube gel electrophoresis; or capillary gel electrophoresis.

5.　　(currently amended) The method of claim 4, wherein the electrophoresis detection apparatus is a ~~MegaBACE~~ capillary sequencing machine.

6.　　(currently amended) <u>A method of assessing the reliability of assigned basecalls in a nucleic acid sequence determination, comprising:</u>

　　　　<u>determining a nucleic acid sequence in accordance with the method of claim 1; and</u>

　　　　[The method of claim 1, further comprising the step of] generating at least one quality score for at least one basecall.

7.　　(original) The method of claim 6, wherein the at least one quality score is a gap-quality score, wherein the gap-quality score estimates the probability of a deletion error between two adjacent assigned basecalls.

8.　　(original) The method of claim 7, wherein the gap-quality score measures degree of noise between the two adjacent assigned basecalls and overly wide peak spacing between the two adjacent assigned basecalls.

9.　　(original) The method of claim 6, further comprising the step of using the quality scores for quality filtering whereby basecalls can be removed or added from the sequence of the nucleic acid polymer during the quality filtering.

10.　　(original) The method of claim 1, wherein the DNA sequencing reactions utilize dye-terminator or dye-primer chemistry.

11.   (original) A computer program product comprising a machine readable medium on which is provided program instructions for determining a sequence of a nucleic acid polymer, the instructions comprising:

code for obtaining data traces from a plurality of channels of an electrophoresis detection apparatus, each channel detecting the products of a DNA sequencing reactions;

code for combining the data traces by a process comprising the steps of:

(i)   applying a cross-correlation coefficient to each of the four data traces to yield four refined traces, wherein the cross-correlation coefficient compares each of the traces with an ideal, Gaussian-shaped peak and wherein the refined traces have narrower peaks than the corresponding data traces;

(ii)   combining the four refined traces to yield a composite trace;

code for detecting peaks in the composite trace by a process that is independent of peak spacing; and

code for determining the sequence of the nucleic acid polymer by assigning basecalls to the peaks.

12.   (original) The computer program product of claim 11, wherein the data traces have been preprocessed.

13.   (original) The computer program product of claim 12, wherein preprocessing comprises the steps of:

(i)   obtaining unprocessed data traces from a plurality of channels of an automated electrophoresis detection apparatus, each channel detecting the products of a DNA sequencing reactions;

(ii)   identifying begin and end points in the unprocessed data;

(iii)   establishing a baseline in the unprocessed data,

(iv)   subtracting the baseline from the unprocessed data to generate the baseline-corrected data; and

(v)   separating the baseline-corrected data to generate the data traces, the separating step comprising spectral or leakage separation.

ICYTP011   4
09/927,321

14.   (original) The computer program product of claim 11, wherein the electrophoresis detection apparatus uses slab gel electrophoresis; tube gel electrophoresis; or capillary gel electrophoresis.

15.   (currently amended) The computer program product of claim 14, wherein the electrophoresis detection apparatus is a ~~MegaBACE~~ capillary sequencing machine.

16.   (currently amended) <u>A computer program product comprising a machine readable medium on which is provided program instructions for assessing the reliability of assigned basecalls in a nucleic acid sequence determination, the instructions comprising:</u>

        <u>program instructions for determining a sequence of a nucleic acid polymer in accordance with claim 11; and</u>

[The computer program product of claim 11, further comprising] code for generating at least one quality score for at least one basecall.

17.   (original) The computer program product of claim 16 wherein the at least one quality score is a gap-quality score, wherein the gap-quality score estimates the probability of a deletion error between two adjacent assigned basecalls.

18.   (original) The computer program product of claim 17, wherein the gap-quality score measures degree of noise between the two adjacent assigned basecalls and overly wide peak spacing between the two adjacent assigned basecalls.

19.   (original) The computer program product of claim 16, further comprising code for using the quality scores for quality filtering whereby basecalls can be removed or added from the sequence of the nucleic acid polymer during the quality filtering.

20.   (original) A computing device comprising a memory device configured to store at least temporarily program instructions for determining a sequence of a nucleic acid polymer, the instructions comprising:

code for obtaining data traces from a plurality of channels of an electrophoresis detection apparatus, each channel detecting the products of a DNA sequencing reactions;

code for combining the data traces by a process comprising the steps of:

(i)   applying a cross-correlation coefficient to each of the four data traces to yield four refined traces, wherein the cross-correlation coefficient compares each of the traces with an ideal, Gaussian-shaped peak and wherein the refined traces have narrower peaks than the corresponding data traces;

(ii)   combining the four refined traces to yield a composite trace;

code for detecting peaks in the composite trace by a process that is independent of peak spacing; and

code for determining the sequence of the nucleic acid polymer by assigning basecalls to the peaks.

21.   (original) The computing device of claim 20, wherein the data traces have been preprocessed.

22.   (original) The computing device of claim 21, wherein preprocessing comprises the steps of:

(i)   obtaining unprocessed data traces from a plurality of channels of an automated electrophoresis detection apparatus, each channel detecting the products of a DNA sequencing reactions;

(ii)   identifying begin and end points in the unprocessed data;

(iii)   establishing a baseline in the unprocessed data,

(iv)   subtracting the baseline from the unprocessed data to generate the baseline-corrected data; and

(v)   separating the baseline-corrected data to generate the data traces, the separating step comprising spectral or leakage separation.

23.   (original) The computing device of claim 20, wherein the electrophoresis detection

apparatus uses slab gel electrophoresis; tube gel electrophoresis; or capillary gel electrophoresis.

24.   (currently amended) The computing device of claim 23, wherein the electrophoreis detection apparatus is a ~~MegaBACE~~ capillary sequencing machine.

25.   (currently amended) <u>A computing device comprising a memory device configured to store at least temporarily program instructions for assessing the reliability of assigned basecalls in a nucleic acid sequence determination, the instructions comprising:</u>

        <u>program instructions for determining a sequence of a nucleic acid polymer in accordance with claim 20; and</u>

        [The computing device of claim 20, further comprising] code for generating at least one quality score for at least one basecall.

26.   (original) The computing device of claim 25, wherein the at least one quality score is a gap-quality score, wherein the gap-quality score estimates the probability of a deletion error between two adjacent assigned basecalls.

27.   (original) The computing device of claim 26, wherein the gap-quality score measures degree of noise between the two adjacent assigned basecalls and overly wide peak spacing between the two adjacent assigned basecalls.

28.   (original) The computing device of claim 25, further comprising code for using the quality scores for quality filtering whereby basecalls can be removed or added from the sequence of the nucleic acid polymer during the quality filtering.

29-61. (cancelled)